



IFW16

RAW SEQUENCE LISTING

DATE: 09/09/2004

PATENT APPLICATION: US/10/035,091B

TIME: 10:51:25

Input Set : A:\Revised Sequence Listing.txt

Output Set: N:\CRF4\09092004\J035091B.raw

3 <110> APPLICANT: Stratagene
 5 <120> TITLE OF INVENTION: HIGH FIDELITY DNA POLYMERASE COMPOSITIONS AND USES THEREFOR
 7 <130> FILE REFERENCE: 25436/2152
 9 <140> CURRENT APPLICATION NUMBER: 10/035,091B
 10 <141> CURRENT FILING DATE: 2001-12-21
 12 <160> NUMBER OF SEQ ID NOS: 11
 14 <170> SOFTWARE: PatentIn version 3.1
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 7
 18 <212> TYPE: PRT
 19 <213> ORGANISM: Artificial Sequence
 21 <220> FEATURE:
 22 <223> OTHER INFORMATION: Conserved domain
 24 <220> FEATURE:
 25 <221> NAME/KEY: MISC_FEATURE
 26 <222> LOCATION: (2)..(3)
 27 <223> OTHER INFORMATION: Conserved domain, X at position 2 or 3 is any amino acid.
 30 <400> SEQUENCE: 1



W--> 32 Asp Xaa Xaa Ser Leu Tyr Pro

33 1 5
 36 <210> SEQ ID NO: 2
 37 <211> LENGTH: 9
 38 <212> TYPE: PRT
 39 <213> ORGANISM: Artificial Sequence -
 41 <220> FEATURE:
 42 <223> OTHER INFORMATION: Conserved domain
 44 <220> FEATURE:
 45 <221> NAME/KEY: MISC_FEATURE
 46 <222> LOCATION: (2)..(7)
 47 <223> OTHER INFORMATION: Conserved domain, X at position 2, 3, 4, or 7 is any amino acid.

50 <400> SEQUENCE: 2

W--> 52 Lys Xaa Xaa Xaa Asn Ser Xaa Tyr Gly

53 1 5
 56 <210> SEQ ID NO: 3
 57 <211> LENGTH: 5
 58 <212> TYPE: PRT
 59 <213> ORGANISM: Artificial Sequence
 61 <220> FEATURE:
 62 <223> OTHER INFORMATION: Conserved domain
 64 <220> FEATURE:
 65 <221> NAME/KEY: misc_feature
 66 <222> LOCATION: (2)..(3)
 67 <223> OTHER INFORMATION: Conserved domain, X at position 2 or 3 is any amino acid.

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70 <400> SEQUENCE: 3
W--> 72 Thr Xaa Xaa Gly Arg
73 1 5
76 <210> SEQ ID NO: 4
77 <211> LENGTH: 6
78 <212> TYPE: PRT
79 <213> ORGANISM: Artificial Sequence
81 <220> FEATURE:
82 <223> OTHER INFORMATION: Conserved domain
84 <220> FEATURE:
85 <221> NAME/KEY: MISC_FEATURE
86 <222> LOCATION: (2)..(2)
87 <223> OTHER INFORMATION: Conserved domain, X at position 2 is any amino acid.
90 <400> SEQUENCE: 4
W--> 92 Tyr Xaa Asp Thr Asp Ser
93 1 5
96 <210> SEQ ID NO: 5
97 <211> LENGTH: 3
98 <212> TYPE: PRT
99 <213> ORGANISM: Artificial Sequence
101 <220> FEATURE:
102 <223> OTHER INFORMATION: Conserved domain
104 <220> FEATURE:
105 <221> NAME/KEY: misc_feature
106 <222> LOCATION: (2)..(2)
107 <223> OTHER INFORMATION: Conserved domain, X at position 2 is any amino acid.
110 <400> SEQUENCE: 5
W--> 112 Lys Xaa Tyr
113 1
116 <210> SEQ ID NO: 6
117 <211> LENGTH: 4
118 <212> TYPE: PRT
119 <213> ORGANISM: Artificial Sequence
121 <220> FEATURE:
122 <223> OTHER INFORMATION: Conserved domain
124 <220> FEATURE:
125 <221> NAME/KEY: MISC_FEATURE
126 <222> LOCATION: (2)..(2)
127 <223> OTHER INFORMATION: Conserved domain, X at position 2 is any amino acid.
130 <400> SEQUENCE: 6
W--> 132 Tyr Xaa Gly Gly
133 1
136 <210> SEQ ID NO: 7
137 <211> LENGTH: 6
138 <212> TYPE: PRT
139 <213> ORGANISM: Artificial Sequence
141 <220> FEATURE:
142 <223> OTHER INFORMATION: Conserved domain
144 <220> FEATURE:

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145 <221> NAME/KEY: MISC_FEATURE
146 <222> LOCATION: (1)..(6)
147 <223> OTHER INFORMATION: Conserved domain
150 <400> SEQUENCE: 7
152 Ser Tyr Thr Gly Gly Phe
153 1 5
156 <210> SEQ ID NO: 8
157 <211> LENGTH: 23
158 <212> TYPE: DNA
159 <213> ORGANISM: Artificial Sequence
161 <220> FEATURE:
162 <223> OTHER INFORMATION: Synthetic primer
164 <220> FEATURE:
165 <221> NAME/KEY: misc_feature
166 <222> LOCATION: (1)..(23)
167 <223> OTHER INFORMATION: Synthetic primer
170 <400> SEQUENCE: 8
171 gaggagagca ggaaaggtgg aag 23
174 <210> SEQ ID NO: 9
175 <211> LENGTH: 23
176 <212> TYPE: DNA
177 <213> ORGANISM: Artificial Sequence
179 <220> FEATURE:
180 <223> OTHER INFORMATION: Synthetic primer
182 <220> FEATURE:
183 <221> NAME/KEY: misc_feature
184 <222> LOCATION: (1)..(23)
185 <223> OTHER INFORMATION: Synthetic primer
188 <400> SEQUENCE: 9
189 gaggtacagg gttgaggcta ctg 23
192 <210> SEQ ID NO: 10
193 <211> LENGTH: 776
194 <212> TYPE: PRT
195 <213> ORGANISM: Thermococcus sp. JDF-3
197 <400> SEQUENCE: 10
199 Met Ile Leu Asp Val Asp Tyr Ile Thr Glu Asn Gly Lys Pro Val Ile
200 1 5 10 15
203 Arg Val Phe Lys Lys Glu Asn Gly Glu Phe Arg Ile Glu Tyr Asp Arg
204 20 25 30
207 Glu Phe Glu Pro Tyr Phe Tyr Ala Leu Leu Arg Asp Asp Ser Ala Ile
208 35 40 45
211 Glu Glu Ile Lys Lys Ile Thr Ala Glu Arg His Gly Arg Val Val Lys
212 50 55 60
215 Val Lys Arg Ala Glu Lys Val Lys Lys Lys Phe Leu Gly Arg Ser Val
216 65 70 75 80
219 Glu Val Trp Val Leu Tyr Phe Thr His Pro Gln Asp Val Pro Ala Ile
220 85 90 95
223 Arg Asp Lys Ile Arg Lys His Pro Ala Val Ile Asp Ile Tyr Glu Tyr
224 100 105 110

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227 Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
228      115      120      125
231 Met Glu Gly Glu Glu Glu Leu Lys Leu Met Ser Phe Asp Ile Glu Thr
232      130      135      140
235 Leu Tyr His Glu Gly Glu Glu Phe Gly Thr Gly Pro Ile Leu Met Ile
236 145      150      155      160
239 Ser Tyr Ala Asp Glu Ser Glu Ala Arg Val Ile Thr Trp Lys Lys Ile
240      165      170      175
243 Asp Leu Pro Tyr Val Glu Val Val Ser Thr Glu Lys Glu Met Ile Lys
244      180      185      190
247 Arg Phe Leu Arg Val Val Lys Glu Lys Asp Pro Asp Val Leu Ile Thr
248      195      200      205
251 Tyr Asn Gly Asp Asn Phe Asp Phe Ala Tyr Leu Lys Lys Arg Cys Glu
252      210      215      220
255 Lys Leu Gly Val Ser Phe Thr Leu Gly Arg Asp Gly Ser Glu Pro Lys
256 225      230      235      240
259 Ile Gln Arg Met Gly Asp Arg Phe Ala Val Glu Val Lys Gly Arg Val
260      245      250      255
263 His Phe Asp Leu Tyr Pro Val Ile Arg Arg Thr Ile Asn Leu Pro Thr
264      260      265      270
267 Tyr Thr Leu Glu Ala Val Tyr Glu Ala Val Phe Gly Lys Pro Lys Glu
268      275      280      285
271 Lys Val Tyr Ala Glu Glu Ile Ala Thr Ala Trp Glu Thr Gly Glu Gly
272      290      295      300
275 Leu Glu Arg Val Ala Arg Tyr Ser Met Glu Asp Ala Arg Val Thr Tyr
276 305      310      315      320
279 Glu Leu Gly Arg Glu Phe Phe Pro Met Glu Ala Gln Leu Ser Arg Leu
280      325      330      335
283 Ile Gly Gln Gly Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
284      340      345      350
287 Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
288      355      360      365
291 Pro Asn Lys Pro Asp Glu Arg Glu Leu Ala Arg Arg Arg Gly Gly Tyr
292      370      375      380
295 Ala Gly Gly Tyr Val Lys Glu Pro Glu Arg Gly Leu Trp Asp Asn Ile
296 385      390      395      400
299 Val Tyr Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr His
300      405      410      415
303 Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Arg Ser Tyr Asp
304      420      425      430
307 Val Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly Phe
308      435      440      445
311 Ile Pro Ser Leu Leu Gly Asn Leu Leu Glu Glu Arg Gln Lys Ile Lys
312      450      455      460
315 Arg Lys Met Lys Ala Thr Leu Asp Pro Leu Glu Lys Asn Leu Leu Asp
316 465      470      475      480
319 Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Tyr Tyr Gly Tyr
320      485      490      495
323 Tyr Gly Tyr Ala Arg Ala Arg Trp Tyr Cys Arg Glu Cys Ala Glu Ser

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324          500          505          510
327 Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Met Val Ile Arg Glu Leu
328          515          520          525
331 Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ala Asp Thr Asp Gly Leu
332          530          535          540
335 His Ala Thr Ile Pro Gly Ala Asp Ala Glu Thr Val Lys Lys Lys Ala
336 545          550          555          560
339 Met Glu Phe Leu Asn Tyr Ile Asn Pro Lys Leu Pro Gly Leu Leu Glu
340          565          570          575
343 Leu Glu Tyr Glu Gly Phe Tyr Val Arg Gly Phe Phe Val Thr Lys Lys
344          580          585          590
347 Lys Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Thr Thr Arg Gly Leu
348          595          600          605
351 Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln Ala
352          610          615          620
355 Arg Val Leu Glu Ala Ile Leu Arg His Gly Asp Val Glu Glu Ala Val
356 625          630          635          640
359 Arg Ile Val Arg Glu Val Thr Glu Lys Leu Ser Lys Tyr Glu Val Pro
360          645          650          655
363 Pro Glu Lys Leu Val Ile His Glu Gln Ile Thr Arg Glu Leu Lys Asp
364          660          665          670
367 Tyr Lys Ala Thr Gly Pro His Val Ala Ile Ala Lys Arg Leu Ala Ala
368          675          680          685
371 Arg Gly Val Lys Ile Arg Pro Gly Thr Val Ile Ser Tyr Ile Val Leu
372          690          695          700
375 Lys Gly Ser Gly Arg Ile Gly Asp Arg Ala Ile Pro Phe Asp Glu Phe
376 705          710          715          720
379 Asp Pro Thr Lys His Lys Tyr Asp Ala Asp Tyr Tyr Ile Glu Asn Gln
380          725          730          735
383 Val Leu Pro Ala Val Glu Arg Ile Leu Arg Ala Phe Gly Tyr Arg Lys
384          740          745          750
387 Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Gly Ala Trp
388          755          760          765
391 Leu Lys Pro Lys Gly Lys Lys Lys
392          770          775
395 <210> SEQ ID NO: 11
396 <211> LENGTH: 2331
397 <212> TYPE: DNA
398 <213> ORGANISM: Thermococcus sp. JDF-3
400 <400> SEQUENCE: 11
401 atgataccttg acgttgatta catcaccgag aatggaaagc ccgtcatcag ggtcttcaag 60
403 aaggagaacg gcgagttcag gattgaatac gaccgcgagt tcgagcccta cttctacgcg 120
405 ctcttcaggg acgactctgc catcgaagaa atcaaaaaga taaccgcgga gaggcacggc 180
407 agggctcgta aggttaagcg cgcggagaag gtgaagaaaa agttcctcgg caggtctgtg 240
409 gaggtctggg tcctctactt cagcacccg caggacgttc cggcaatccg cgacaaaata 300
411 aggaagcacc ccgcggtcat cgacatctac gagtacgaca tacccttcgc caagcgctac 360
413 ctcatagaca agggcctaata cccgatggaa ggtgaggaag agcttaaaact catgtccttc 420
415 gacatcgaga cgctctacca cgagggagaa gagtttggaa ccgggccgat tctgatgata 480
417 agctacgccg atgaaagcga ggcgcgcgtg ataacctgga agaagatcga ccttccttac 540

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/035,091B

DATE: 09/09/2004
TIME: 10:51:26

Input Set : A:\Revised Sequence Listing.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. ~~2,3~~
Seq#:2; Xaa Pos. ~~2,3,4,7~~
Seq#:3; Xaa Pos. ~~2,3~~
Seq#:4; Xaa Pos. ~~2~~
Seq#:5; Xaa Pos. ~~2~~
Seq#:6; Xaa Pos. ~~2~~

VERIFICATION SUMMARY

DATE: 09/09/2004

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Input Set : A:\Revised Sequence Listing.txt

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L:32 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:52 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:72 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:92 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:112 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0